

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/664,958A  
Source: IFW16  
Date Processed by STIC: 10/21/05

# ***ENTERED***



IFW

IFW16

## RAW SEQUENCE LISTING

DATE: 10/21/2005

PATENT APPLICATION: US/09/664,958A

TIME: 09:05:44

Input Set : A:\60240 SeqList 10.14.05.ST25.txt

Output Set: N:\CRF4\10212005\I664958A.raw

3 <110> APPLICANT: The Trustees of Columbia University in the City of New York  
 4 Trakht, Ilya  
 5 Canfield, Robert  
 6 Kalantarov, Gary  
 7 Rudchenko, Sergei  
 9 <120> TITLE OF INVENTION: Novel Tumor-Associated Marker  
 11 <130> FILE REFERENCE: 0575/60240/JPW/AJM/AJD  
 13 <140> CURRENT APPLICATION NUMBER: 09/664,958A  
 -> 14 <141> CURRENT FILING DATE: 2000-09-18  
 16 <160> NUMBER OF SEQ ID NOS: 53  
 18 <170> SOFTWARE: PatentIn version 3.3  
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 21 <211> LENGTH: 333  
 22 <212> TYPE: PRT  
 23 <213> ORGANISM: Human  
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 32 20 25 30  
 35 Gly Pro Leu Gly Gly Gly Gly Ser Gly Gly Pro Gln Met Gly Leu Pro  
 36 35 40 45  
 39 Pro Pro Pro Pro Ala Leu Arg Pro Arg Leu Val Phe His Thr Gln Leu  
 40 50 55 60  
 43 Ala His Gly Ser Pro Thr Gly Arg Ile Glu Gly Phe Thr Asn Val Lys  
 44 65 70 75 80  
 47 Glu Leu Tyr Gly Lys Ile Ala Glu Ala Phe Arg Leu Pro Thr Ala Glu  
 48 85 90 95  
 51 Val Met Phe Cys Thr Leu Asn Thr His Lys Val Asp Met Asp Lys Leu  
 52 100 105 110  
 55 Leu Gly Gly Gln Ile Gly Leu Glu Asp Phe Ile Phe Ala His Val Lys  
 56 115 120 125  
 59 Gly Gln Arg Lys Glu Val Glu Val Phe Lys Ser Glu Asp Ala Leu Gly  
 60 130 135 140  
 63 Leu Thr Ile Thr Asp Asn Gly Ala Gly Tyr Ala Phe Ile Lys Arg Ile  
 64 145 150 155 160  
 67 Lys Glu Gly Ser Val Ile Asp His Ile His Leu Ile Ser Val Gly Asp  
 68 165 170 175  
 71 Met Ile Glu Ala Ile Asn Gly Gln Ser Leu Leu Gly Cys Arg His Tyr  
 72 180 185 190  
 75 Glu Val Ala Arg Leu Leu Lys Glu Leu Pro Arg Gly Arg Thr Phe Thr  
 76 195 200 205  
 79 Leu Lys Leu Thr Glu Pro Arg Lys Ala Phe Asp Met Ile Ser Gln Arg

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80      210      215      220
83 Ser Ala Gly Gly Arg Pro Gly Ser Gly Pro Gln Leu Gly Thr Gly Arg
84 225      230      235      240
87 Gly Thr Leu Arg Leu Arg Ser Arg Gly Pro Ala Thr Val Glu Asp Leu
88      245      250      255
91 Pro Ser Ala Phe Glu Glu Lys Ala Ile Glu Lys Val Asp Asp Leu Leu
92      260      265      270
95 Glu Ser Tyr Met Gly Ile Arg Asp Thr Glu Leu Ala Ala Thr Met Val
96      275      280      285
99 Glu Leu Gly Lys Asp Lys Arg Asn Pro Asp Glu Leu Ala Glu Ala Leu
100      290      295      300
103 Asp Glu Arg Leu Gly Asp Phe Ala Phe Pro Asp Glu Phe Val Phe Asp
104 305      310      315      320
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121 cccctctag tggaaaatga ggaggctgag ccaggccgtg gagggctggg cgtgggggag 180
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127 cgcacgagg gggtcaccaa cgtcaaggag ctgtatggca agattgccga ggccttccgc 360
129 ctgccaaactg ccgaggtgat gttttgcacc ctgaacaccc acaaagtgga catggacaag 420
131 ctcttggggg gccaaatcgg gctggaggac ttcatcttcg ccacgtgaa ggggcagcgc 480
133 aaggagggtg aggtgttcaa gtcggaggat gcactcgggc tcaccatcac ggacaacggg 540
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137 atcagcgtgg gcgacatgat cgaggccatt aacgggcaga gcctgctggg ctgccggcac 660
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Output Set: N:\CRF4\10212005\I664958A.raw

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174 gcccagacatg ggggaaccccg ggcccaggcg tgtgtgtcac catgacaaca gagacaggcc      180
176 ccgactctga ggtgaagaaa gctcaggagg agggcccgca gcagcccgag gctgtgtccg      240
178 ctgtgaccac ccctgtgacc cctgcaggcc acggccaccc agaggccaac tccaatgaga      300
180 agcatccatc ccagcaggac acgcggcctg ctgaacagag cctagacatg gaggagaagg      360
182 actacagtga ggccgatggc ctttcggaga ggaccacgcc cagcaaggcc cagaaatcgc      420
184 cccagaagat tgccaagaaa tacaagagtg ccatctgccg ggctactctg cttgatgcct      480
186 cggagtatga gtgtgagggt gagaaacatg gccggggcca ggtgctgttt gacctggtct      540
188 gtgaacacct caacctccta gagaaggact acttcggcct gaccttctgt gatgtgaca      600
190 gccagaagaa ctggctggac ccctccaagg agatcaagaa gcagatccgg agtagccct      660
192 ggaattttgc cttcacagtc aagtctctacc cgctgatcc tgcccagctg acagaagaca      720
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196 gctcctttgt cacgcatgcc ctactgggct cctacgctgt gcaggctgag ctgggtgact      840
198 atgatgctga ggagcatgtg ggcaactatg tcagcgagct ccgcttcgcc cctaaccaga      900
200 cccgggagct ggaggagagg atcatggagc tgcataagac atataggggg atgaccccg      960
202 gagaagcaga aatccacttc ttagagaatg ccaagaagct ttccatgtac ggagtagacc      1020
204 tgcaccatgc caaggactct gagggcatcg acatcatgtt aggcgtttgt gccaatggcc      1080
206 tgetcatcta ccgggaccgg ctgagaatca accgctttgc ctggcccaag atcctcaaga      1140
208 tctcctacaa gaggagtaac ttctatatca agatccggcc tggggagtat gagcaatttg      1200
210 agagcacaat tggttttaag ctcccaaacc accggtcagc caagagactg tggaaggtct      1260
212 gcacgagca tcatacattc ttccggctgg tgtccctga gccccaccc aagggttcc      1320
214 tgggtgatgg cccaagttc cggtagctg ggagagccca ggcacagact cgccaggcca      1380
216 gcgccctcat tgaccggcct gcacccttct ttgagcgttc ttccagcaaa cggtagacca      1440
218 tgtcccgtag ccttgatgga gcagagttct cccgcccagc ctcggtcagc gagaacctg      1500
220 atgcagggcc tgacggtgac aagcgggatg aggatggcga gtctgggggg caacggtcag      1560
222 aggtgagga gggagagggtc aggaactcaa ccaagatcaa ggagctaaag ccggagcagg      1620
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232 aagtcaaacc accacgtccc cgggccccag agagtgacac aggcgatgag gaccaggacc      1920
234 aggagaggga cacggtgttc ctgaaggaca accacctggc cattgagcgc aagtgtcca      1980
236 gcatcacggt cagctctacg tctagcctgg aggtgaggt ggacttcacg gtcattggtg      2040
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240 aaagcgactc ggacactgag ggctgctgt tctcccgga tctcaacaag ggggccccca      2160
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268	gaagggaaaa	gcatatatat	atagatatat	agagatatag	atatatatac	aggaaacacc	3000
270	gcatecttgc	actgctgctg	gggctggcag	agcagttggc	tgacagcaac	aaccgacatc	3060
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276	caagccagac	cacgatgatt	gtagaagtcc	ctcccgcctt	ggttctgcac	gttacagtta	3240
278	gcagacgagc	aattccattt	gttcttctcc	agcatctcta	aggccacttt	gaatgcaaag	3300
280	gaaaacactt	gcacagcaaa	gcaagagaag	tcacagcagc	aagacacgca	cagtcaacca	3360
282	ttttccgaga	aaaaaagaaa	attccccact	tggaaagaaa	gaggaggaac	actggattct	3420
284	tactttctgg	atcttgacac	tgggtgcaa	aacctacctt	cctctctccc	gcctcccttc	3480
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356	cgagggagga	ggggacctgc	aaagctagaa	tctagggcac	tgtttcctcc	ccatccttct	5640
358	ctttgtagag	aatagagacg	tttgtcttgt	ctgtcttcaa	cctacttttc	cttttctctt	5700
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366 ataagcagaa agaaccagat gctctccagg gtctttttct actttgctat ctcattgggtc 5940
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374 ctgtcctgtt ccttttttact cacacccttc tctcctttct cgtccccatg cccccccacc 6180
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397 35 40 45
400 Gly Val Leu Val Thr Met Thr Thr Glu Thr Gly Pro Asp Ser Glu Val
401 50 55 60
404 Lys Lys Ala Gln Glu Glu Ala Pro Gln Gln Pro Glu Ala Ala Ala Ala
405 65 70 75 80
408 Val Thr Thr Pro Val Thr Pro Ala Gly His Gly His Pro Glu Ala Asn
409 85 90 95
412 Ser Asn Glu Lys His Pro Ser Gln Asp Thr Arg Pro Ala Glu Gln Ser
413 100 105 110
416 Leu Asp Met Glu Glu Lys Asp Tyr Ser Glu Ala Asp Gly Leu Ser Glu
417 115 120 125
420 Arg Thr Thr Pro Ser Lys Ala Gln Lys Ser Pro Gln Lys Ile Ala Lys
421 130 135 140
424 Lys Tyr Lys Ser Ala Ile Cys Arg Val Thr Leu Leu Asp Ala Ser Glu
425 145 150 155 160
428 Tyr Glu Cys Glu Val Glu Lys His Gly Arg Gly Gln Val Leu Phe Asp
429 165 170 175
432 Leu Val Cys Glu His Leu Asn Leu Leu Glu Lys Asp Tyr Phe Gly Leu
433 180 185 190
436 Thr Phe Cys Asp Ala Asp Ser Gln Lys Asn Trp Leu Asp Pro Ser Lys
437 195 200 205
440 Glu Ile Lys Lys Gln Ile Arg Ser Ser Pro Trp Asn Phe Ala Phe Thr
441 210 215 220
444 Val Lys Phe Tyr Pro Pro Asp Pro Ala Gln Leu Thr Glu Asp Ile Thr
445 225 230 235 240
448 Arg Tyr Tyr Leu Cys Leu Gln Leu Arg Ala Asp Ile Ile Thr Gly Arg
449 245 250 255
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453 260 265 270
456 Gln Ala Glu Leu Gly Asp Tyr Asp Ala Glu Glu His Val Gly Asn Tyr

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Base Note:

a of n and/or Xaa have been detected in the Sequence Listing. Please review the  
quence Listing to ensure that a corresponding explanation is presented in the <220>  
<223> fields of each sequence which presents at least one n or Xaa.

1#:15; N Pos. 23,42,48,1105

1#:17; N Pos. 23,42

## VERIFICATION SUMMARY

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14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

1689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0

341 Repeated in SeqNo=15

1810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0